

Sequences producing significant alignments:

Peptide

Score E
(bits) Value

gi 22416427 qb AAM96215.1	potassium-chloride transporter-3...	1226	0.0	G
gi 6693798 qb AAF24986.1	K-Cl cotransporter KCC3 [Homo sap...	1226	0.0	G
gi 33329252 qb AAQ10026.1	K-Cl cotransporter KCC3a-X2M iso...	1208	0.0	G
gi 41281645 ref NP_598410.1	solute carrier family 12, memb...	1197	0.0	G
gi 47124056 qb AAH70107.1	SLC12A6 protein [Homo sapiens]	1184	0.0	G
gi 33329256 qb AAQ10028.1	K-Cl cotransporter KCC3a-S2 isof...	1183	0.0	G
gi 38565928 qb AAH62099.1	Unknown (protein for MGC:69652) ...	1157	0.0	
gi 22416428 qb AAM96216.1	potassium-chloride transporter-3...	1154	0.0	G
gi 19526769 ref NP_598409.1	solute carrier family 12, memb...	1134	0.0	G
gi 34856648 ref XP_342490.1	similar to K-Cl cotransporter ...	1117	0.0	G
gi 7512561 pir T17275	hypothetical protein DKFZp434D2135.1...	1116	0.0	G
gi 19110891 qb AAL85335.1	K-Cl cotransporter KCC3 variant ...	1115	0.0	G
gi 9507107 ref NP_062102.1	solute carrier family 12, membe...	865	0.0	G
gi 45219767 qb AAH66872.1	Solute carrier family 12, member...	862	0.0	G
gi 27151684 sp Q28677 S124	RABIT Solute carrier family 12 m...	862	0.0	
gi 6677993 ref NP_033221.1	solute carrier family 12, membe...	862	0.0	G

gi 4827006 ref NP_005063.1 	solute carrier family 12 (potas...	862	0.0	G
gi 47213488 emb CAF91145.1 	unnamed protein product [Tetrao...	859	0.0	
gi 31324218 gb AAP47188.1 	potassium-chloride cotransporter...	856	0.0	G
gi 47522728 ref NP_999114.1 	K-Cl cotransporter [Sus scrofa...	856	0.0	G
gi 3015641 gb AAC39685.1 	erythroid K:Cl cotransporter spli...	837	0.0	G
gi 11968148 ref NP_065759.1 	solute carrier family 12 membe...	783	0.0	G
gi 19705463 ref NP_599190.1 	solute carrier family 12 membe...	783	0.0	G
gi 12003227 gb AAG43493.1 	electroneutral potassium-chlorid...	783	0.0	G
gi 14193696 gb AAK56093.1 	K-Cl cotransporter [Mus musculus...	780	0.0	G
gi 28972652 dbj BAC65742.1 	mKIAA1176 protein [Mus musculus]	780	0.0	G
gi 3015639 gb AAC39684.1 	erythroid K:Cl cotransporter spli...	780	0.0	G
gi 33859680 ref NP_065066.1 	solute carrier family 12, memb...	778	0.0	G
gi 6755534 ref NP_035520.1 	solute carrier family 12, membe...	773	0.0	G
gi 47847414 dbj BAD21379.1 	mFLJ00098 protein [Mus musculus]	773	0.0	G
gi 6330233 dbj BAA86490.1 	KIAA1176 protein [Homo sapiens]	772	0.0	G
gi 5730043 ref NP_006589.1 	solute carrier family 12 (potas...	767	0.0	G
gi 50753670 ref XP_414082.1 	PREDICTED: similar to K-Cl cot...	766	0.0	G
gi 50733496 ref XP_418891.1 	PREDICTED: similar to mFLJ0009...	761	0.0	G
gi 32490535 gb AAP84988.1 	potassium-chloride cotransporter...	753	0.0	
gi 47225214 emb CAF98841.1 	unnamed protein product [Tetrao...	753	0.0	
gi 9651224 gb AAF91094.1 	K-Cl cotransporter KCC1 [Mus musc...	707	0.0	G
gi 47223173 emb CAG11308.1 	unnamed protein product [Tetrao...	688	0.0	
gi 47220725 emb CAG11794.1 	unnamed protein product [Tetrao...	687	0.0	
gi 47213000 emb CAF95392.1 	unnamed protein product [Tetrao...	672	0.0	
gi 24762439 ref NP_726378.1 	CG5594-PA [Drosophila melanoga...	598	e-169	G
gi 21429886 gb AAM50621.1 	GH09271p [Drosophila melanogaste...	597	e-169	G
gi 46409210 gb AAS93762.1 	LD02554p [Drosophila melanogaste...	595	e-168	G
gi 22026947 ref NP_571976.2 	CG5594-PC [Drosophila melanoga...	594	e-168	G
gi 10440500 dbj BAB15783.1 	FLJ00098 protein [Homo sapiens]	531	e-149	G
gi 48096020 ref XP_394587.1 	similar to CG5594-PC [Apis mel...	531	e-149	G
gi 10440514 dbj BAB15787.1 	FLJ00105 protein [Homo sapiens]	501	e-140	G
gi 34853395 ref XP_217744.2 	similar to putative potassium-...	452	e-125	G
gi 25149428 ref NP_500910.2 	solute carrier family 12 membe...	440	e-121	G
gi 39584234 emb CAE61609.1 	Hypothetical protein CBG05529 [...	438	e-121	
gi 31226974 ref XP_317803.1 	ENSANGP00000014479 [Anopheles ...	420	e-115	G
gi 17541928 ref NP_501141.1 	solute carrier family 12 membe...	360	2e-97	G
gi 39593544 emb CAE61836.1 	Hypothetical protein CBG05808 [...	353	2e-95	
gi 26343083 dbj BAC35198.1 	unnamed protein product [Mus mu...	332	3e-89	
gi 18073139 emb CAC80545.1 	putative Na-K-Cl cotransporter ...	322	4e-86	
gi 39596034 emb CAE67537.1 	Hypothetical protein CBG13060 [...	320	1e-85	
gi 31226957 ref XP_317800.1 	ENSANGP00000004794 [Anopheles ...	311	8e-83	G
gi 13507237 gb AAK28520.1 	K-Cl cotransporter [Xenopus laevis]	309	3e-82	
gi 17534831 ref NP_495555.1 	Na-K-Cl cotransporter (2H716) ...	299	3e-79	G
gi 32484273 gb AAH54325.1 	LOC398663 protein [Xenopus laevis]	224	8e-57	G
gi 31226979 ref XP_317804.1 	ENSANGP00000024771 [Anopheles ...	208	8e-52	G
gi 50944163 ref XP_481609.1 	putative Na ⁺ /K ⁺ /Cl-cotransport...	206	4e-51	
gi 15208177 dbj BAB63113.1 	hypothetical protein [Macaca fa...	202	4e-50	
gi 2582381 gb AAC49874.1 	cation-chloride co-transporter [N...	201	1e-49	
gi 9651629 gb AAF91220.1 	potassium-chloride cotransporter ...	200	2e-49	

gi 47193414 emb CAG14039.1	unnamed protein product [Tetrao...	194	2e-47	
gi 30691724 ref NP_849732.1	cation-chloride cotransporter,...	194	2e-47	G
gi 6634764 gb AAF19744.1	Strong similarity to gb AF021220 ...	192	4e-47	
gi 47203569 emb CAG13773.1	unnamed protein product [Tetrao...	187	1e-45	
gi 3582769 gb AAC35282.1	erythrocyte K-Cl cotransporter [H...	183	3e-44	G
gi 9651216 gb AAF91090.1	K-Cl cotransporter [Mus musculus]	165	6e-39	G
gi 3925714 emb CAA09464.1	KCC2 protein [Mus musculus]	153	3e-35	G
gi 14043556 gb AAH07760.1	SLC12A7 protein [Homo sapiens]	149	6e-34	G
gi 35505532 gb AAH57624.1	Slc12a5 protein [Mus musculus]	147	2e-33	G
gi 31226967 ref XP_317802.1	ENSANGP00000015001 [Anopheles ...	141	9e-32	G
gi 7512576 pir T17231	hypothetical protein DKFZp434F076.1 ...	136	4e-30	G
gi 20151457 gb AAM11088.1	GH27027p [Drosophila melanogaste...	133	3e-29	G
gi 52075682 dbj BAD44902.1	putative potassium-chloride cot...	130	2e-28	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	130	3e-28	
gi 50778569 ref XP_427392.1	PREDICTED: similar to solute c...	127	2e-27	G
gi 48119195 ref XP_393214.1	similar to bumetanide sensitiv...	123	3e-26	G
gi 34905658 ref NP_914176.1	putative cation-chloride co-tr...	121	1e-25	G
gi 1673531 gb AAB18960.1	furosemide-sensitive K-Cl cotrans...	120	2e-25	
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransporte...	111	1e-22	
gi 31236589 ref XP_319440.1	ENSANGP00000014326 [Anopheles ...	111	1e-22	G
gi 13937397 ref NP_113583.1	solute carrier family 12 (pota...	106	4e-21	G
gi 51859114 gb AAH81728.1	Cation-chloride cotransporter 6 ...	105	9e-21	G
gi 13516498 dbj BAB40456.1	cation chloride cotransporter 6...	105	9e-21	G
gi 51094566 gb EAL23818.1	solute carrier family 12 (potass...	104	2e-20	G
gi 9502260 gb AAF88060.1	cation-chloride cotransporter-int...	103	2e-20	G
gi 6179898 gb AAF05702.1	Na+/K+/2Cl- cotransporter [Callin...	101	1e-19	
gi 14486416 gb AAK62044.1	Na+/K+/2Cl- cotransporter [Carci...	101	1e-19	
gi 48101446 ref XP_395129.1	similar to ENSANGP00000014326 ...	100	2e-19	G
gi 13383504 gb AAK21009.1	cation-chloride cotransporter-in...	100	2e-19	
gi 50423949 ref XP_460559.1	unnamed protein product [Debar...	100	3e-19	G
gi 31242251 ref XP_321556.1	ENSANGP00000011560 [Anopheles ...	100	4e-19	G
gi 19705533 ref NP_599232.1	cation-chloride cotransporter ...	99	5e-19	G
gi 25304083 gb AAH40138.1	Unknown (protein for MGC:48843) ...	98	1e-18	
gi 516001 gb AAC48592.1	bumetanide-sensitive Na-K-Cl cotra...	97	2e-18	
gi 1709296 sp P55015 S121	RABIT Solute carrier family 12 me...	97	3e-18	
gi 95071103 ref NP_062007.1	solute carrier family 12, membe...	97	3e-18	G
gi 4557849 ref NP_000329.1	sodium potassium chloride cotra...	97	3e-18	G
gi 1079521 gb AAC52633.1	kidney-specific Na-K-Cl cotranspo...	97	3e-18	G
gi 2290526 gb AAB65150.1	Na-(K)-Cl cotransporter isoform m...	97	3e-18	G
gi 6755532 ref NP_035519.1	solute carrier family 12, membe...	96	7e-18	G
gi 34365781 ref NP_899197.1	solute carrier family 12, memb...	96	7e-18	G
gi 16877251 gb AAH16888.1	Solute carrier family 12, member...	96	7e-18	G
gi 27151793 sp P55014 S121	MOUSE Solute carrier family 12 m...	96	7e-18	G
gi 40950187 gb AAR97733.1	Na-K-Cl cotransporter [Oreochrom...	96	7e-18	
gi 17543066 ref NP_502704.1	solute carrier family 12 membe...	95	1e-17	G
gi 47230656 emb CAF99849.1	unnamed protein product [Tetrao...	95	1e-17	
gi 21483278 gb AAM52614.1	GH09711p [Drosophila melanogaste...	95	1e-17	G
gi 20177071 gb AAM12297.1	RH37201p [Drosophila melanogaster]	95	1e-17	
gi 24644255 ref NP_730939.1	CG31547-PA [Drosophila melanog...	95	1e-17	G

gi 39586961 emb CAE62896.1	Hypothetical protein CBG07084 [...	94	3e-17	
gi 2136942 pir I46497	bumetanide-sensitive Na-K-Cl cotrans...	93	5e-17	
gi 27652641 emb CAD31111.1	putative sodium-potassium-chlor...	93	5e-17	
gi 2137580 pir I49269	Na+/K+/Cl-cotransport protein renal ...	93	5e-17	G
gi 47224809 emb CAG06379.1	unnamed protein product [Tetrao...	92	1e-16	
gi 50752967 ref XP_413814.1	PREDICTED: similar to bumetani...	91	1e-16	G
gi 15010508 gb AAK77302.1	GH08340p [Drosophila melanogaste...	91	2e-16	G
gi 31197669 ref XP_307782.1	ENSANGP00000012928 [Anopheles ...	91	2e-16	G
gi 23955920 gb AAN40689.1	putative sodium-potassium-2-chlo...	91	2e-16	
gi 47227672 emb CAG09669.1	unnamed protein product [Tetrao...	91	2e-16	
gi 40950185 gb AAR97732.1	Na-K-Cl cotransporter [Oreochrom...	91	2e-16	
gi 47210716 emb CAF92943.1	unnamed protein product [Tetrao...	90	4e-16	
gi 27652643 emb CAD31112.1	putative sodium-potassium-chlor...	89	5e-16	
gi 40950183 gb AAR97731.1	Na-K-Cl cotransporter [Oreochrom...	89	5e-16	
gi 21686589 gb AAM74968.1	renal Na-K-Cl cotransporter isof...	89	7e-16	
gi 21686587 gb AAM74967.1	renal Na-K-Cl cotransporter isof...	89	7e-16	
gi 47213642 emb CAF90346.1	unnamed protein product [Tetrao...	89	9e-16	
gi 596076 gb AAA75600.1	bumetanide sensitive NaK2Cl cotran...	88	1e-15	
gi 17535967 ref NP_493773.1	cation-chloride cotransporter-...	88	2e-15	G
gi 50727039 gb AAT81190.1	Hypothetical protein T04B8.5b [C...	88	2e-15	
gi 50344814 ref NP_001002080.1	zgc:85961 [Danio rerio] >gi...	88	2e-15	G
gi 4506977 ref NP_000330.1	solute carrier family 12 (sodiu...	87	3e-15	G
gi 1717801 sp P55017 S123 HUMAN	Solute carrier family 12 me...	87	3e-15	G
gi 7513175 pir G01202	NaCl electroneutral Thiazide-sensiti...	87	3e-15	G
gi 5759119 gb AAD50984.1	Na-K-2Cl- cotransporter [Oryctola...	87	3e-15	
gi 1083802 pir B54145	sodium-chloride transporter, Thiazid...	86	4e-15	
gi 33563368 ref NP_062218.2	solute carrier family 12, memb...	86	4e-15	G
gi 21686585 gb AAM74966.1	renal Na-K-Cl cotransporter isof...	86	6e-15	
gi 21686583 gb AAM74965.1	renal Na-K-Cl cotransporter isof...	86	6e-15	
gi 2599070 gb AAC33139.1	thiazide-sensitive sodium chlorid...	86	6e-15	
gi 2136267 pir PC4180	thiazide-sensitive sodium-chloride c...	86	8e-15	
gi 38073244 gb AAR10806.1	K-Cl cotransporter KCC3b isoform...	85	1e-14	
gi 14547897 ref NP_062288.1	solute carrier family 12, memb...	85	1e-14	G
gi 24047306 gb AAH38612.1	Solute carrier family 12, member...	85	1e-14	G
gi 30721813 gb AAP33906.1	bumetanide-sensitive Na-K-Cl cot...	84	2e-14	G
gi 6677991 ref NP_033220.1	solute carrier family 12, membe...	84	2e-14	G
gi 2147143 pir I51307	basolateral Na(+)-K(+)-Cl- cotranspo...	84	2e-14	
gi 1709294 sp P55013 S122 SQUAC	Solute carrier family 12 me...	84	3e-14	
gi 34879509 ref XP_346514.1	hypothetical protein XP_346513...	84	3e-14	G
gi 27807511 ref NP_777207.1	solute carrier family 12 (sodi...	84	3e-14	G
gi 13929130 ref NP_113986.1	solute carrier family 12, memb...	84	3e-14	G
gi 50761390 ref XP_424716.1	PREDICTED: similar to Solute c...	84	3e-14	G
gi 5081312 gb AAD39342.1	bumetanide-sensitive Na-K-2Cl cot...	84	3e-14	G
gi 47222533 emb CAG02898.1	unnamed protein product [Tetrao...	83	4e-14	
gi 50753599 ref XP_414059.1	PREDICTED: similar to solute c...	83	5e-14	G
gi 48102011 ref XP_392732.1	similar to CG4357-PA [Apis mel...	81	1e-13	G
gi 290856 gb AAA49272.1	thiazide sensitine NaCl cotranspor...	80	2e-13	
gi 1581614 prf 2117156A	basolateral Na/K/Cl cotransporter	80	2e-13	
gi 4584410 emb CAB40708.1	basolateral NaK(2Cl) cotransport...	78	2e-12	
gi 46441770 gb EAL01065.1	hypothetical protein CaO19.6833 ...	76	5e-12	
gi 34857570 ref XP_345417.1	similar to K-Cl cotransporter ...	75	8e-12	G
gi 21686581 gb AAM74964.1	renal Na-K-Cl cotransporter isof...	75	8e-12	
gi 21686579 gb AAM74963.1	renal Na-K-Cl cotransporter isof...	75	8e-12	

gi 46100179 gb EAK85412.1	hypothetical protein UM04602.1 [...	74	2e-11	
gi 47226271 emb CAG09239.1	unnamed protein product [Tetrao...	72	1e-10	
gi 37575103 gb AAQ93478.1	furosemide-sensitive KCl cotrans...	71	2e-10	
gi 46446456 ref YP_007821.1	putative bumetanide-sensitive ...	70	3e-10	G
gi 44984445 gb AAS53347.1	AFL025Cp [Eremothecium gossypii]...	70	3e-10	G
gi 50292197 ref XP_448531.1	unnamed protein product [Candi...	70	3e-10	G
gi 6319712 ref NP_009794.1	Hypothetical ORF; Ybr235wp [Sac...	70	4e-10	G
gi 50545908 ref XP_500492.1	hypothetical protein [Yarrowia...	69	6e-10	G
gi 50311073 ref XP_455560.1	unnamed protein product [Kluyv...	69	6e-10	G
gi 19112532 ref NP_595740.1	putative membrane transporter ...	69	7e-10	G
gi 45527020 ref ZP_00178221.1	COG0531: Amino acid transpor...	67	2e-09	
gi 17533079 ref NP_495469.1	cation-chloride cotransporter ...	67	4e-09	G
gi 48893479 ref ZP_00326715.1	COG0531: Amino acid transpor...	65	8e-09	
gi 32404944 ref XP_323085.1	hypothetical protein (AL5134...	65	1e-08	G
gi 47013799 gb AAT08445.1	Na-K-Cl cotransporter isoform 2 ...	64	2e-08	
gi 38073242 gb AAR10805.1	K-Cl cotransporter KCC4 [Rattus ...	64	2e-08	G
gi 24899633 ref NP_705889.1	cation-chloride cotransporter ...	64	2e-08	G
gi 23495278 dbj BAC20265.1	cation-chloride cotransporter 9...	64	2e-08	G
gi 19527414 ref NP_599012.1	solute carrier family 12, memb...	64	3e-08	G
gi 39582293 emb CAE67542.1	Hypothetical protein CBG13067 [...	64	3e-08	
gi 21411274 gb AAH30926.1	Slc12a8 protein [Mus musculus]	63	4e-08	G
gi 20892349 ref XP_147174.1	cation-chloride cotransporter ...	63	4e-08	
gi 10440502 dbj BAB15784.1	FLJ00100 protein [Homo sapiens]	63	4e-08	G
gi 10440351 dbj BAB15711.1	FLJ00010 protein [Homo sapiens]	63	4e-08	G
gi 42551588 gb EAA74431.1	hypothetical protein FG05147.1 [...	62	7e-08	G
gi 48140542 ref XP_397130.1	similar to CG12773-PA [Apis me...	62	1e-07	G
gi 20093291 ref NP_619366.1	Na-K-Cl cotransporter [Methano...	61	2e-07	G
gi 47013797 gb AAT08444.1	Na-K-Cl cotransporter isoform 1 ...	61	2e-07	
gi 45523845 ref ZP_00175172.1	COG0531: Amino acid transpor...	61	2e-07	
gi 39581643 emb CAE71764.1	Hypothetical protein CBG18756 [...	61	2e-07	
gi 16417791 gb AAL18853.1	potassium chloride cotransporter...	60	3e-07	
gi 47202516 emb CAF87431.1	unnamed protein product [Tetrao...	60	3e-07	
gi 4185298 gb AAD09008.1	Na-K-2Cl cotransporter [Rattus no...	60	3e-07	G
gi 16588876 gb AAL26926.1	thiazide-sensitive Na-Cl cotrans...	60	4e-07	
gi 12652805 gb AAH00154.1	SLC12A9 protein [Homo sapiens]	59	6e-07	G
gi 50750706 ref XP_422105.1	PREDICTED: similar to solute c...	59	6e-07	G
gi 38107570 gb EAA53722.1	hypothetical protein MG09472.4 [...	59	6e-07	G
gi 37906389 gb AAP44496.1	Na-K-Cl cotransporter [Aedes aeg...	59	6e-07	
gi 38569457 ref NP_078904.3	solute carrier family 12, memb...	59	8e-07	G
gi 21666316 gb AAM73657.1	solute carrier family 12 member ...	59	8e-07	G
gi 28628359 gb AAQ49174.1	cation-chloride cotransporter 9 ...	59	8e-07	G
gi 47209879 emb CAF91324.1	unnamed protein product [Tetrao...	59	1e-06	
gi 15281553 gb AAK94307.1	solute carrier family 12 member ...	57	2e-06	G
gi 51476920 emb CAH18426.1	hypothetical protein [Homo sapi...	57	2e-06	
gi 31216859 ref XP_316315.1	ENSANGP00000020551 [Anopheles ...	57	3e-06	G
gi 40741631 gb EAA60821.1	hypothetical protein AN4478.2 [A...	57	3e-06	G
gi 33589522 gb AAQ22528.1	LD15480p [Drosophila melanogaste...	57	4e-06	G
gi 33327540 gb AAQ09093.1	SLC12A8 cation-chloride cotransp...	55	8e-06	G
gi 3127109 gb AAC16048.1	Na-K-Cl cotransporter BSC2 [Rattu...	52	7e-05	G

gi 15789485 ref NP_279309.1 	cationic amino acid transporte...	<u>52</u>	1e-04	G
gi 79644 pir S06903	hypothetical protein 128 - Synechococc...	<u>51</u>	2e-04	
gi 26342949 dbj BAC35131.1 	unnamed protein product [Mus mu...	<u>50</u>	4e-04	G
gi 31321986 gb AAM48576.1 	RHAG-2 [Takifugu rubripes]	<u>50</u>	5e-04	G
gi 21226632 ref NP_632554.1 	Amino acid permease [Methanosa...	<u>46</u>	0.005	G
gi 26992100 gb AAN86742.1 	Na-K-Cl cotransporter homolog [R...	<u>46</u>	0.005	
gi 47216974 emb CAG04916.1 	unnamed protein product [Tetrao...	<u>45</u>	0.011	
gi 47201162 emb CAF87719.1 	unnamed protein product [Tetrao...	<u>45</u>	0.011	
gi 31874120 emb CAD97969.1 	hypothetical protein [Homo sapi...	<u>42</u>	0.074	G
gi 6324649 ref NP_014718.1 	t-SNARE that resides on the end...	<u>42</u>	0.096	G
gi 16903173 gb AAK01946.1 	K-Cl cotransporter [Homo sapiens]	<u>40</u>	0.37	G
gi 4584408 emb CAB40707.1 	apical Na(2Cl)K cotransporter [B...	<u>39</u>	0.62	G
gi 48840136 ref ZP_00297064.1 	COG0531: Amino acid transpor...	<u>39</u>	0.81	
gi 16801675 ref NP_471943.1 	similar to amino acid transpor...	<u>39</u>	0.81	G
gi 15922144 ref NP_377813.1 	442aa long conserved hypotheti...	<u>37</u>	3.1	G
gi 50753376 ref XP_413964.1 	PREDICTED: similar to bumetani...	<u>37</u>	3.1	G
gi 14521274 ref NP_126749.1 	hypothetical protein PAB0712 [...	<u>37</u>	4.0	G
gi 46906258 ref YP_012647.1 	membrane protein, putative [Li...	<u>37</u>	4.0	G
gi 45519701 ref ZP_00171252.1 	COG2244: Membrane protein in...	<u>37</u>	4.0	
gi 24374728 ref NP_718771.1 	flagellar biosynthetic protein...	<u>36</u>	5.3	G
gi 33236849 gb AAP98936.1 	putative transport permease [Chl...	<u>36</u>	5.3	G
gi 52009842 ref ZP_00337204.1 	COG4177: ABC-type branched-c...	<u>36</u>	5.3	
gi 48862094 ref ZP_00315992.1 	COG0167: Dihydroorotate dehy...	<u>36</u>	6.9	
gi 20089515 ref NP_615590.1 	antigen [Methanosarcina acetiv...	<u>36</u>	6.9	G
gi 45382387 ref NP_990203.1 	SOCS box-containing WD protein...	<u>36</u>	6.9	G
gi 50411673 ref XP_457068.1 	unnamed protein product [Debar...	<u>36</u>	6.9	G
gi 47095094 ref ZP_00232706.1 	membrane protein, putative [...	<u>36</u>	6.9	
gi 20143912 ref NP_599027.1 	WD SOCS-box protein 1 isoform ...	<u>35</u>	9.0	G
gi 18677720 ref NP_056441.6 	WD SOCS-box protein 1 isoform ...	<u>35</u>	9.0	G
gi 22760676 dbj BAC11291.1 	unnamed protein product [Homo s...	<u>35</u>	9.0	G
gi 47096061 ref ZP_00233662.1 	amino acid permease family p...	<u>35</u>	9.0	
gi 6563198 gb AAF17193.1 	WSB-1 protein [Homo sapiens] >gi ...	<u>35</u>	9.0	G

Alignments

Get selected sequences

Select all

Deselect all

☐ >[gi|22416427|gb|AAM96215.1|](#) **G** potassium-chloride transporter-3a [Homo sapiens]
[gi|5106523|gb|AAD39742.1|](#) **G** K-Cl cotransporter KCC3a [Homo sapiens]
[gi|27151690|sp|Q9UHW9|S126](#) HUMAN **G** Solute carrier family 12 member 6 (Electroneut
cotransporter 3) (K-Cl cotransporter 3)
Length = 1150

Score = 1226 bits (3173), Expect = 0.0

Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLXXXXXXXXXXXXXXXXXXXXXXXXTSRXXXX 60
MHPPETTTKMASVRFMVTPTKIDDIPGL TSR
Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRS--- 57

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Query: 61  XXXXXXXXXXXLSQNSGHHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED----- 111
              E M      GATTSLATVAL      RTSHPQDVIED
Sbjct: 58  -----EPMSEMGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD-----QRNAYLNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156
            ITGEHSQLLDD      RNAYLNNSNYE  +E FDKNLA      KVSSLLNRMA
Sbjct: 96  SITGEHSQLLDDGHHKARNAYLNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157  NY----QGAKEHEEAENITNLXXXXXXXXXXXXXQMG-----LQNI FGVT FMGVYILFLRL 207
            NY      QGAKEHEEAENIT      MG      LQNI FGVT      ILFLRL
Sbjct: 155  NYTNLTQGAKEHEEAENITEGKKKPTKTPQMGT FMGVYLPCLQNI FGVT-----ILFLRL 208

Query: 208  LPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 267
            TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
Sbjct: 209  ---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 262

Query: 268  TTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAA 315
            EFGGAVGLCF      AAAMYILGAI      IVPRAAIFHSDDALKESAA
Sbjct: 263  -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313

Query: 316  MLNNMRVYGT AFLVLMVLVVF IGVRVYVNFASXFLACVIVSILAIYAGAIKSSFAPPHFP 375
            MLNNMRVYGT AFLVLMVLVVF IGVRVYVNFAS FLACVIVSILAIYAGAIKSSFAPPHFP
Sbjct: 314  MLNNMRVYGT AFLVLMVLVVF IGVRVYVNFASLFLACVIVSILAIYAGAIKSSFAPPHFP 373

Query: 376  VCMLGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSSYFVHN 421
            VCMLGNRTLSS IDVCSKTKEINNMT VPSK      NATCDE      YFVHN
Sbjct: 374  VCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHN 427

Query: 422  NVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIE----KSSDVLGSLNHEYVLVDPSAK 477
            NV      TSIQGIPGLASGIITENLWSNYLPKGEIIE      KSSDVLGSLNHEYVLVD
Sbjct: 428  NV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---- 480

Query: 478  ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS LWGFF FVYLSNV 537
            ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS      FVYLSNV
Sbjct: 481  ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNV 535

Query: 538  VLFGACIEGVVLRDKFG-----VGTLSWP-----SFFSTCGAGDAVKGNLVPPWV 581
            VLFGACIEGVVLRDKFG      VGTLSWP      SFFSTCGAG
Sbjct: 536  VLFGACIEGVVLRDKFGDAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582  IVIGSLQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626
            LQSL      TGAP      RLLQAIK      VFGHSKANGEPT
Sbjct: 585  -----LQSL-----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTA 627

Query: 627  -----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666
            GILIASLD      FFLMCYLF L      CALQ
Sbjct: 628  AIAELGILIASLDLVAPILSMFFLMCYLFVN-----ACALQTLRLTPN 671

Query: 667  -----RYYHWALSFMG MTPNWNLARPRPRFSICLALMF-----IVAMVIAGMIGA EK 714
            RYYHWALSFMG M      SICLALMF      IVAMVIAGM
Sbjct: 672  WRPRFRYYHWALSFMG M-----SICLALMFISSWYYAIVAMVIAGM----- 712

Query: 715  SSWYYAIYKXIEYQSLSPHTDEDEWGDGI---XXXXXXXXXXXXXEEGP---KNWRPQXXX 768
            IYK IEYQ      E EWGDGI      EEGP      KNWRPQ
Sbjct: 713  -----IYKIEYQGA-----EKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLV 761

Query: 769  XXXXXX-----XXXTFASQLKGNFLHV KAGKGXTIVG SVIV-----GEALAAEQTI 814
            TFASQL      KAGKG TIVG SVIV      GEALAAEQTI
Sbjct: 762  LLKLDEDLHV KHPRLLT FASQL-----KAGKGLTIVG SVIVGNFLENYGEALAAEQTI 814

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Query: 815 KHVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGW 864
 KH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV MGW
 Sbjct: 815 KH-----LMEAEKVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV----MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSNVEQFSEG-- 919
 PNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG
 Sbjct: 861 PNGWRQSE----DARAWKTFIGTVR-----VTTAAHLALLVAKNISFFPSNVEQFSEGN 911

Query: 920 -VWVIVHDGGMLML---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRIE 969
 VWVIVHDGGMLML LLKQHKVWRK TVAQLEDNSI + ATFLYHLRIE
 Sbjct: 912 DVWVIVHDGGMLMLLPFLLKQHKVWRKCSIRIFTVAQLEDNSIQMKKDL-ATFLYHLRIE 970

Query: 970 AEVRIFKDLEVVRTLEMHSDISAYTYERHMRLSKMMEQRSQML-----TERDRIAQL 1022
 AEV + +EMHSDISAYTYER + MMEQRSQML TERDR AQL
 Sbjct: 971 AEVEV-----VEMHSDISAYTYERTL----MMEQRSQMLRHMRLSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXXXXXXMAQDLLHTAVYQEKVHM-----SRGQ 1073
 VKDRNSMLRLTSIGS T YQEKVHM SRGQ
 Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQEKVHMTWTKDKYMASRGQ 1060

Query: 1074 KAKSMEGF----NMRPDQSNVRRM---KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1125
 KAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN
 Sbjct: 1061 KAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDEN 1120

Query: 1126 YMEFLEVLTXXXXXXXXXXXXXXSEVITIYS 1155
 YMEFLEVL SEVITIYS
 Sbjct: 1121 YMEFLEVLTEGLERVLLVRGGGSEVITIYS 1150

☐ >gi|6693798|gb|AAF24986.1| ☒ K-C1 cotransporter KCC3 [Homo sapiens]
 Length = 1150

Score = 1226 bits (3173), Expect = 0.0
 Identities = 835/1350 (61%), Positives = 842/1350 (62%), Gaps = 395/1350 (29%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLXXXXXXXXXXXXXXXXXXXXXXXXTSRXXXX 60
 MHPPETTTKMASVRFMVTPTKIDDIPGL TSR
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESVPETSRS--- 57

Query: 61 XXXXXXXXXXXLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111
 E M GATTSLATVAL RTSHPQDVIED
 Sbjct: 58 -----EPMSEMGGATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFEEESFDKNLA-----KVSSLLNRMA 156
 ITGEHSQLLDD RNAYLNNSNYE +E FDKNLA KVSSLLNRMA
 Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYEE-GDEYFDKNLALFEEEMDTRPKVSSLLNRMA 154

Query: 157 NY----QGAKEHEEAENITNLXXXXXXXXXXXXXQMG-----LQNI FGVTFMGVYILFLRL 207
 NY QGAKEHEEAENIT MG LQNI FGVT FMGVYILFLRL
 Sbjct: 155 NYTNLTQGAKEHEEAENITEGKKKPTKTPQMGTFMGVYLPCLQNI FGVT----ILFLRL 208

Query: 208 LPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 267
 TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
 Sbjct: 209 ---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP--- 262

Query: 268 TTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAA 315
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAA
 Sbjct: 263 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAA 313

Query: 316 MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHFP 375
MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHFP
Sbjct: 314 MLNNMRVYGTAFVLMLVLFVFIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHFP 373

Query: 376 VCMLGNRTLSS--IDVCSKTKEINNMT--VPSK-----NATCDECNSSYFVHN 421
VCMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE YFVHN
Sbjct: 374 VCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHN 427

Query: 422 NVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIE---KSSDVLGSLNHEYVLVDPSAK 477
NV TSIQGIPGLASGIITENLWSNYLPKGEIIE KSSDVLGSLNHEYVLVD
Sbjct: 428 NV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---- 480

Query: 478 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFFVYLSNV 537
ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FVYLSNV
Sbjct: 481 ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FVYLSNV 535

Query: 538 VLFGACIEGVVLRDKFG-----VGTLSWP-----SFFSTCGAGDAVKGNLVPWV 581
VLFGACIEGVVLRDKFG VGTLSWP SFFSTCGAG
Sbjct: 536 VLFGACIEGVVLRDKFGDAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAG----- 584

Query: 582 IVIGSLQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626
LQSL TGAP RLLQAIK VFGHSKANGEPT
Sbjct: 585 -----LQSL-----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLTA 627

Query: 627 -----GILIASLD-----FFLMCYLFTLLRLTAALVAPIAELILSMCALQ----- 666
GILIASLD FFLMCYLF L CALQ
Sbjct: 628 AIAELGILIASLDLVAPILSMFFLMCYLFVN-----ACALQTLRLTPN 671

Query: 667 -----RYYHWALSFMGMTNWNLARPRPRFSICLALMF-----IVAMVIAGMIGAEK 714
RYYHWALSFMGMT SICLALMF IVAMVIAGM
Sbjct: 672 WRPRFRYYHWALSFMGMT-----SICLALMFISSWYYAIVAMVIAGM----- 712

Query: 715 SSWYYAIYKXIEYQSLSPHTDEDEWGDGI---XXXXXXXXXXXXXEEGP---KNWRPQXXX 768
IYK IEYQ E EWGDGI EEGP KNWRPQ
Sbjct: 713 -----IYKYIEYQGA-----EKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLV 761

Query: 769 XXXXXX-----XXXTFASQLKGNFLHVKAGKGXTIVGSVIV-----GEALAAEQTI 814
TFASQL KAGKG TIVGSVIV GEALAAEQTI
Sbjct: 762 LLKLDEDLHVKHPRLLTFASQL-----KAGKGLTIVGSVIVGNFLHNYGEALAAEQTI 814

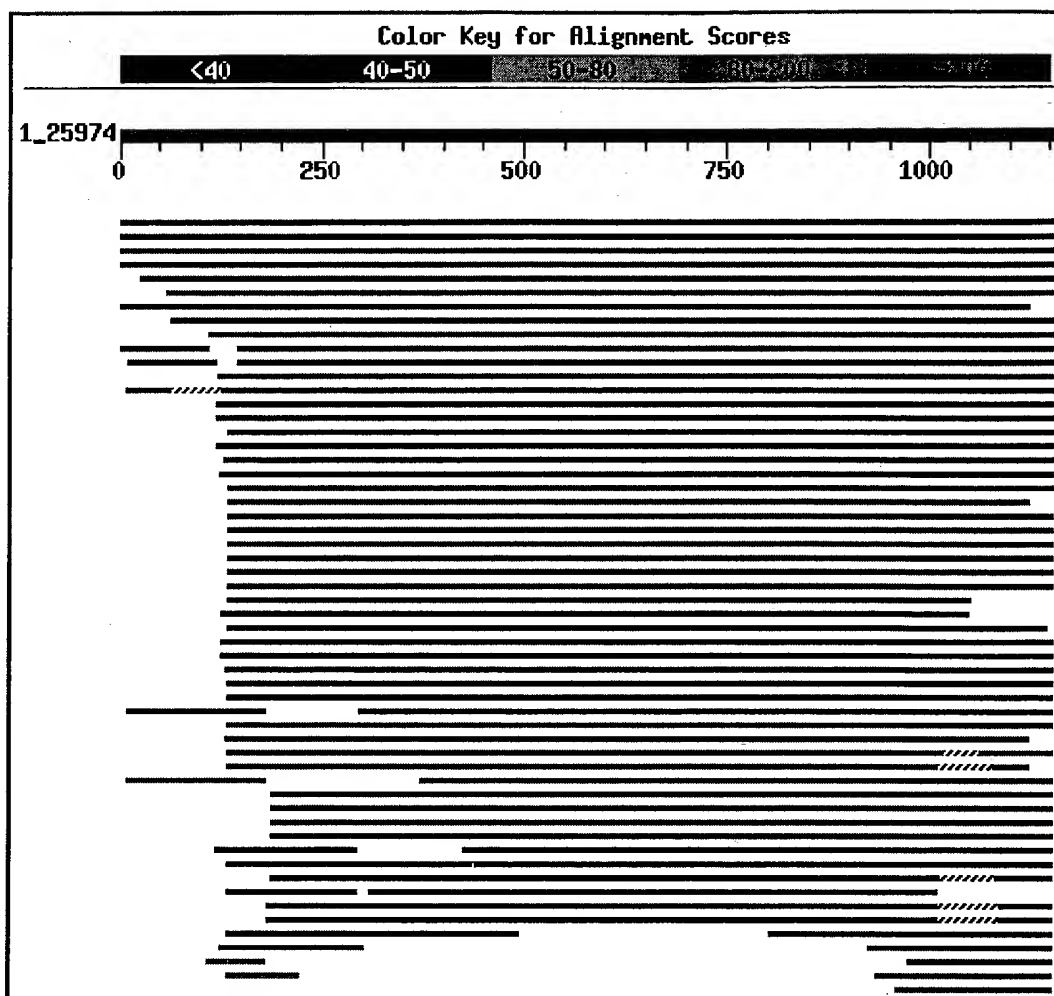
Query: 815 KHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNTVVLIQSMGW 864
KH LMEAEKVKGFCQL AKLREGISH GGMKHNTVV MGW
Sbjct: 815 KH-----LMEAEKVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV----MGW 860

Query: 865 PNGWRQSERVTTDARAWKTFIGTVKNINIDLFFAAHLALLVA---SFFPSNVEQFSEG-- 919
PNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG
Sbjct: 861 PNGWRQSE----DARAWKTFIGTVR-----VTTAAHLALLVAKNISFFPSNVEQFSEGN 911

Query: 920 -VWWIVHDGGMMLL---LLKQHKVWRK-----TVAQLEDNSISCSIQMKATFLYHLRIE 969
VWWIVHDGGMMLL LLKQHKVWRK TVAQLEDNSI + ATFLYHLRIE
Sbjct: 912 DVWWIVHDGGMMLLPFLLLKQHKVWRKCSIRIFTVAQLEDNSIQMKKDL-ATFLYHLRIE 970

Query: 970 AEVRIKFDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQML-----TERDRIAQL 1022
AEV + +EMHDSDISAYTYER + MMEQRSQML TERDR AQL
Sbjct: 971 AEVEV-----VEMHDSDISAYTYERTL---MMEQRSQMLRHMRLSKTERDREAQL 1017

Query: 1023 VKDRNSMLRLTSIGSXXXXXXXXXXXXXXXXXMAQDLLHTAVYQEKVHM-----SRGQ 1073
VKDRNSMLRLTSIGS T YQEKVHM SRGQ
Sbjct: 1018 VKDRNSMLRLTSIGSDEDE-----ETETYQEKVHMTWTKDKYMASRGQ 1060



Sequences producing significant alignments:

Score	E
(bits)	Value

gi 22416427 gb AAM96215.1 	potassium-chloride transporter-3...	2531	0.0	G
gi 6693798 gb AAF24986.1 	K-Cl cotransporter KCC3 [Homo sap...	2531	0.0	G
gi 33329252 gb AAQ10026.1 	K-Cl cotransporter KCC3a-X2M iso...	2499	0.0	G
gi 41281645 ref NP_598410.1 	solute carrier family 12, memb...	2466	0.0	G
gi 47124056 gb AAH70107.1 	SLC12A6 protein [Homo sapiens]	2444	0.0	G
gi 33329256 gb AAQ10028.1 	K-Cl cotransporter KCC3a-S2 isof...	2350	0.0	G
gi 38565928 gb AAH62099.1 	Unknown (protein for MGC:69652) ...	2345	0.0	
gi 22416428 gb AAM96216.1 	potassium-chloride transporter-3...	2294	0.0	G
gi 19526769 ref NP_598409.1 	solute carrier family 12, memb...	2246	0.0	G
gi 19110891 gb AAL85335.1 	K-Cl cotransporter KCC3 variant ...	2221	0.0	G
gi 7512561 pir T17275	hypothetical protein DKFZp434D2135.1...	2221	0.0	G
gi 34856648 ref XP_342490.1 	similar to K-Cl cotransporter ...	2212	0.0	G
gi 47213488 emb CAF91145.1 	unnamed protein product [Tetrao...	1646	0.0	
gi 9507107 ref NP_062102.1 	solute carrier family 12, membe...	1620	0.0	G
gi 6677993 ref NP_033221.1 	solute carrier family 12, membe...	1614	0.0	G
gi 47522728 ref NP_999114.1 	K-Cl cotransporter [Sus scrofa...	1611	0.0	G

gi 45219767 gb AAH66872.1	Solute carrier family 12, member...	1611	0.0	G
gi 27151684 sp Q28677 S124	RAB1T Solute carrier family 12 m...	1608	0.0	
gi 31324218 gb AAP47188.1	potassium-chloride cotransporter...	1607	0.0	G
gi 4827006 ref NP_005063.1	solute carrier family 12 (potas...	1602	0.0	G
gi 3015641 gb AAC39685.1	erythroid K:Cl cotransporter spli...	1511	0.0	G
gi 19705463 ref NP_599190.1	solute carrier family 12 membe...	1431	0.0	G
gi 11968148 ref NP_065759.1	solute carrier family 12 membe...	1426	0.0	G
gi 14193696 gb AAK56093.1	K-Cl cotransporter [Mus musculus...	1426	0.0	G
gi 33859680 ref NP_065066.1	solute carrier family 12, memb...	1426	0.0	G
gi 12003227 gb AAG43493.1	electroneutral potassium-chlorid...	1426	0.0	G
gi 28972652 dbj BAC65742.1	mKIAA1176 protein [Mus musculus]	1426	0.0	G
gi 3015639 gb AAC39684.1	erythroid K:Cl cotransporter spli...	1415	0.0	G
gi 50753670 ref XP_414082.1	PREDICTED: similar to K-Cl cot...	1413	0.0	G
gi 6330233 dbj BAA86490.1	KIAA1176 protein [Homo sapiens]	1398	0.0	G
gi 5730043 ref NP_006589.1	solute carrier family 12 (potas...	1378	0.0	G
gi 47225214 emb CAF98841.1	unnamed protein product [Tetrao...	1374	0.0	
gi 50733496 ref XP_418891.1	PREDICTED: similar to mFLJ0009...	1373	0.0	G
gi 6755534 ref NP_035520.1	solute carrier family 12, membe...	1365	0.0	G
gi 47847414 dbj BAD21379.1	mFLJ00098 protein [Mus musculus]	1365	0.0	G
gi 9651224 gb AAF91094.1	K-Cl cotransporter KCC1 [Mus musc...	1339	0.0	G
gi 32490535 gb AAP84988.1	potassium-chloride cotransporter...	1318	0.0	
gi 47213000 emb CAF95392.1	unnamed protein product [Tetrao...	1147	0.0	
gi 47220725 emb CAG11794.1	unnamed protein product [Tetrao...	1136	0.0	
gi 47223173 emb CAG11308.1	unnamed protein product [Tetrao...	1113	0.0	
gi 10440500 dbj BAB15783.1	FLJ00098 protein [Homo sapiens]	999	0.0	G
gi 21429886 gb AAM50621.1	GH09271p [Drosophila melanogaste...	985	0.0	G
gi 24762439 ref NP_726378.1	CG5594-PA [Drosophila melanoga...	985	0.0	G
gi 46409210 gb AAS93762.1	LD02554p [Drosophila melanogaste...	974	0.0	G
gi 22026947 ref NP_571976.2	CG5594-PC [Drosophila melanoga...	974	0.0	G
gi 10440514 dbj BAB15787.1	FLJ00105 protein [Homo sapiens]	954	0.0	G
gi 34853395 ref XP_217744.2	similar to putative potassium-...	893	0.0	G
gi 48096020 ref XP_394587.1	similar to CG5594-PC [Apis mel...	843	0.0	G
gi 31226974 ref XP_317803.1	ENSANGP00000014479 [Anopheles ...	644	0.0	G
gi 25149428 ref NP_500910.2	solute carrier family 12 membe...	584	e-165	G
gi 39584234 emb CAE61609.1	Hypothetical protein CBG05529 [...	578	e-163	
gi 13507237 gb AAK28520.1	K-Cl cotransporter [Xenopus laevis]	552	e-155	
gi 26343083 dbj BAC35198.1	unnamed protein product [Mus mu...	490	e-136	
gi 32484273 gb AAH54325.1	LOC398663 protein [Xenopus laevis]	474	e-132	G
gi 15208177 dbj BAB63113.1	hypothetical protein [Macaca fa...	439	e-121	
gi 31226957 ref XP_317800.1	ENSANGP00000004794 [Anopheles ...	421	e-115	G
gi 47203569 emb CAG13773.1	unnamed protein product [Tetrao...	389	e-106	
gi 9651629 gb AAF91220.1	potassium-chloride cotransporter ...	375	e-102	
gi 18073139 emb CAC80545.1	putative Na-K-Cl cotransporter ...	365	5e-99	
gi 38073246 gb AAR10807.1	K-Cl cotransporter KCC3a isoform...	356	4e-96	
gi 17541928 ref NP_501141.1	solute carrier family 12 membe...	329	5e-88	G
gi 35505532 gb AAH57624.1	Slc12a5 protein [Mus musculus]	326	4e-87	G
gi 38073248 gb AAR10808.1	brain-specific K-Cl cotransporte...	324	2e-86	
gi 39596034 emb CAE67537.1	Hypothetical protein CBG13060 [...	296	3e-78	
gi 9651216 gb AAF91090.1	K-Cl cotransporter [Mus musculus]	284	2e-74	G

gi 47193414 emb CAG14039.1	unnamed protein product [Tetrao...	283	4e-74	
gi 7512576 pir T17231	hypothetical protein DKFZp434F076.1 ...	279	4e-73	G
gi 3925714 emb CAA09464.1	KCC2 protein [Mus musculus]	267	2e-69	G
gi 3582769 gb AAC35282.1	erythrocyte K-Cl cotransporter [H...	262	6e-68	G
gi 31226979 ref XP_317804.1	ENSANGP00000024771 [Anopheles ...	261	2e-67	G
gi 14043556 gb AAH07760.1	SLC12A7 protein [Homo sapiens]	252	6e-65	G
gi 17534831 ref NP_495555.1	Na-K-Cl cotransporter (2H716) ...	236	3e-60	G
gi 31226967 ref XP_317802.1	ENSANGP00000015001 [Anopheles ...	230	3e-58	G
gi 34857570 ref XP_345417.1	similar to K-Cl cotransporter ...	229	5e-58	G
gi 37575103 gb AAQ93478.1	furosemide-sensitive KCl cotrans...	221	2e-55	
gi 1673531 gb AAB18960.1	furosemide-sensitive K-Cl cotrans...	217	2e-54	
gi 39593544 emb CAE61836.1	Hypothetical protein CBG05808 [...	216	3e-54	
gi 50778569 ref XP_427392.1	PREDICTED: similar to solute c...	191	2e-46	G
gi 38073244 gb AAR10806.1	K-Cl cotransporter KCC3b isoform...	167	3e-39	
gi 30691724 ref NP_849732.1	cation-chloride cotransporter,...	138	1e-30	G
gi 34905658 ref NP_914176.1	putative cation-chloride co-tr...	134	3e-29	G
gi 50944163 ref XP_481609.1	putative Na+/K+/Cl-cotransport...	133	5e-29	
gi 52075682 dbj BAD44902.1	putative potassium-chloride cot...	132	9e-29	
gi 16417791 gb AAL18853.1	potassium chloride cotransporter...	131	2e-28	
gi 2582381 gb AAC49874.1	cation-chloride co-transporter [N...	123	4e-26	
gi 20151457 gb AAM11088.1	GH27027p [Drosophila melanogaste...	118	1e-24	G
gi 31242251 ref XP_321556.1	ENSANGP00000011560 [Anopheles ...	118	2e-24	G
gi 516001 gb AAC48592.1	bumetanide-sensitive Na-K-Cl cotra...	112	1e-22	
gi 1079521 gb AAC52633.1	kidney-specific Na-K-Cl cotranspo...	112	1e-22	G
gi 2290526 gb AAB65150.1	Na-(K)-Cl cotransporter isoform m...	112	1e-22	G
gi 21686589 gb AAM74968.1	renal Na-K-Cl cotransporter isof...	111	2e-22	
gi 21686587 gb AAM74967.1	renal Na-K-Cl cotransporter isof...	111	2e-22	
gi 25304083 gb AAH40138.1	Unknown (protein for MGC:48843) ...	109	7e-22	
gi 6755532 ref NP_035519.1	solute carrier family 12, membe...	109	7e-22	G
gi 34365781 ref NP_899197.1	solute carrier family 12, memb...	109	7e-22	G
gi 16877251 gb AAH16888.1	Solute carrier family 12, member...	109	7e-22	G
gi 27151793 sp P55014 S121	MOUSE Solute carrier family 12 m...	109	7e-22	G
gi 40950187 gb AAR97733.1	Na-K-Cl cotransporter [Oreochrom...	109	7e-22	
gi 9507103 ref NP_062007.1	solute carrier family 12, membe...	108	2e-21	G
gi 38073242 gb AAR10805.1	K-Cl cotransporter KCC4 [Rattus ...	107	4e-21	G

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|22416427|gb|AAM96215.1| **G** potassium-chloride transporter-3a [Homo sapiens]
gi|5106523|gb|AAD39742.1| **G** K-Cl cotransporter KCC3a [Homo sapiens]
gi|27151690|sp|Q9UHW9|S126 HUMAN **G** Solute carrier family 12 member 6 (Electroneut
cotransporter 3) (K-Cl cotransporter 3)
Length = 1150

Score = 2531 bits (5961), Expect = 0.0

Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60
MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM
Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111
SEMS GATTSLATVAL RTSHPQDVIED
Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPQDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM
Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNIIFGVTFMGVYI 202
ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIIFGV I
Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKTPQMGTFMGVYLPCLQNIIFGV-----I 203

Query: 203 LFLRLLPCTWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
LFLRL TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
Sbjct: 204 LFLRL---TWVVGTAGVLQAFIAVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310
GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL
Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNNMRVYGTAFLVLMVLVVFIVGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370
KESAAMLNNMRVYGTAFLVLMVLVVFIVGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA
Sbjct: 309 KESAAMLNNMRVYGTAFLVLMVLVVFIVGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFVCM LGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416
PPHFVCM LGNRTLSS IDVCSKTKEINNMT VPSK NATCDE
Sbjct: 369 PPHFVCM LGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472
YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLV
Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLV 479

Query: 473 DPSAKITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532
D ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV
Sbjct: 480 D----ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI
Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT-- 626
GS LQSL TGAP RLLQAIK VFGHSKANGEPT
Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664
GILIASLD LVAPI LSM CA
Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI---LSMFFLMCYL FVN LACA 662

Query: 665 LQ-----RYYHWALSFMGMTPNWNLARPRPRFSICLALMFI-----VAMV 705
LQ RYYHWALSFMGM SICLALMFI VAMV
Sbjct: 663 LQTLRTPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGA EKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP--- 759
IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGP PHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG
 Sbjct: 753 KNWRPQLLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855
 EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHNT
 Sbjct: 806 EALAAEQTIKH-----LMEAEKVKGFCQLVVAAKLREGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSN 912
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN
 Sbjct: 856 VV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNISFFPSN 902


Query: 913 VEQFSEG---VWWIVHDGGMMLLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG VWWIVHDGGMMLLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 903 VEQFSEGNI DVWWIVHDGGMMLLLPFL LKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIKDLLEVVRTLEMHDSDISAYTYERHMR LSKMMEQRSQML----- 1013
 ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQML
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL-----MMEQRSQMLRHRMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM- 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF---NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
 Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVL VLRGGGSEVITIYS 1155
 PGPPRNPEGDENYMEFLEVLTEGLERVL VLRGGGSEVITIYS
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVL VLRGGGSEVITIYS 1150

☐ >gi|6693798|gb|AAF24986.1|  K-C1 cotransporter KCC3 [Homo sapiens]
 Length = 1150

Score = 2531 bits (5961), Expect = 0.0

Identities = 926/1362 (67%), Positives = 930/1362 (68%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60
 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDVIED---- 111
 SEMS GATTSLATVAL RTSHPDVIED
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPDVIEDLSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM
 Sbjct: 96 SITGEHSQLLDDGHHKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTGEGKKKPTKTPQMG-----LQNIFGVTFMGVYI 202
 ANY QGAKEHEEAENIT EGKKKPTKTPQMG LQNIFGV I
 Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKTPQMGTFMGVYLPCLQNIFGV-----I 203

Query: 203 LFLRLLPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
 LFLRL TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
 Sbjct: 204 LFLRL---TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310
 GP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDAL

Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDAL 308

Query: 311 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASXFLACVIVSILAIYAGAIKSSFA 370
 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFAS FLACVIVSILAIYAGAIKSSFA

Sbjct: 309 KESAAMLNNMRVYGTAFVLVLMVLVVFVIGVRYVNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPHFVCM LGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416
 PPHFVCM LGNRTLSS IDVCSKTKEINNMT VPSK NATCDE

Sbjct: 369 PPHFVCM LGNRTLSS RHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLV

Sbjct: 423 YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLV 479

Query: 473 DPSAKITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532
 D ITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV

Sbjct: 480 D----ITTSFTLLVGIFFPSTVGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
 YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI

Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT-- 626
 GS LQSL TGAP RLLQAIK VFGHSKANGEPT

Sbjct: 575 GSFFSTCGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664
 GILIASLD LVAPI LSM CA

Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLACA 662

Query: 665 LQ-----RYYHWALSFMGMT PNWVNLRPRPRFSICLALMFI-----VAMV 705
 LQ RYYHWALSFMGMT SICLALMFI VAMV

Sbjct: 663 LQTLRLTPNWRPRFRYYHWALSFMGMT-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGA EKSSWYYAIYKXIEYQSLSPHTDEWDGIRGL---AARFALLRLEEGP--- 759
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP

Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWDGIRGLSLSAARFALLRLEEGPPHT 752

Query: 760 KNWRPQLLVLLKL-----HPRLLT FASQLKGNFLHV KAGKXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLT FASQLK AGKG TIVGSVIVG

Sbjct: 753 KNWRPQLLVLLKLDEDLHV KHPRLLT FASQLK-----AGKGLTIVGSVIVGNFLHNYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855
 EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHNT

Sbjct: 806 EALAAEQTIKH-----LMEAEKVKGFCQLVVA AKLREGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSN 912
 VV MGWPNQSERVTTDARAWKTFIGTV+ + AAHLALLVA SFFPSN

Sbjct: 856 VV----MGWPNQSERVTTDARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGM LMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG VWWIVHDGGM LMLL LKQHKVWRK TVAQLEDNSI QMK

Sbjct: 903 VEQFSEG NIDVWWIVHDGGM LMLLPFL LKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIFKDLEVVRTLEMHDS DISAYTYERHMR LSKMMEQRSQML---- 1013
 ATFLYHLRIEAEV EVV EMHDS DISAYTYER + MMEQRSQML

Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDS DISAYTYERTL----MMEQRSQMLRHMR 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM- 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
 Sbjct: 1049 WTKDKYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS 1155
 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVLVRRGGGSEVITIYS 1150

☐ >gi|33329252|gb|AAQ10026.1| ☒ K-C1 cotransporter KCC3a-X2M isoform [Homo sapiens]
 Length = 1135

Score = 2499 bits (5886), Expect = 0.0

Identities = 916/1356 (67%), Positives = 920/1356 (67%), Gaps = 422/1356 (31%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSRVRFSSRESVPETSRSEPM 60
 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPD SSRSSRVRFSSRESVPETSRSEPM
 Sbjct: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDQDVIEDITGE 115
 SEMS GATTSLATVAL RTSHPDQDVIED
 Sbjct: 61 SEMS-----GATTSLATVALDPPSDRTSHPDQDVIED----- 91

Query: 116 HSQLLDDQ---RNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158
 D RNAYLNNSNYE E +E FDKNLA KVSSLLNRMANY
 Sbjct: 92 -----DGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNI FGVT FMGVYILFLRL 208
 QGAKEHEEAENIT EGKKKPTKTPQMG LQNI FGVT ILFLRL
 Sbjct: 145 TQGAKEHEEAENIT---EGKKKPTKTPQMGT FMGVYLPCLQNI FGVT-----ILFLRL- 193

Query: 209 PCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLG 268
 TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
 Sbjct: 194 --TWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP---- 247

Query: 269 TFEIFLVYEFEGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAAM 316
 EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDALKESAAM
 Sbjct: 248 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAAM 299

Query: 317 LNNMRVYGT AFLVLMVLVVF IGVRVYNKFASXFLACVIVSILAIYAGAIKSSFAPPHFPV 376
 LNNMRVYGT AFLVLMVLVVF IGVRVYNKFAS FLACVIVSILAIYAGAIKSSFAPPHFPV
 Sbjct: 300 LNNMRVYGT AFLVLMVLVVF IGVRVYNKFASLFLACVIVSILAIYAGAIKSSFAPPHFPV 359

Query: 377 CMLGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSSYFVHNN 422
 CMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE YFVHNN
 Sbjct: 360 CMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHNN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKI 478
 V TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVLVD I
 Sbjct: 414 V---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD----I 466

Query: 479 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS LWGFFVYLSNVV 538
 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVV
 Sbjct: 467 TTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVV 521

Query: 539 LFGACIEGVVLRDKFGVGTLSWSPFFSTCGAGDAVKGNLV-----PWVIVIGS---- 586
 LFGACIEGVVLRDKFG DAVKGNLV PWVIVIGS
 Sbjct: 522 LFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWSPWPVIVIGSFFST 565

Query: 587 ----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 566 CGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTAA 613

Query: 627 ----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CALQ---- 666
 GILIASLD LVAPI LSM CALQ
 Sbjct: 614 IAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLACALQTLLR 653

Query: 667 -----RYYHWALSFMGMTPNWNLARPRPRFSICLALMFI-----VAMVIAGMIG 711
 RYYHWALSFMGM SICLALMFI VAMVIAGM
 Sbjct: 654 TPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQ 765
 IYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ
 Sbjct: 698 -----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQ 743

Query: 766 LLVLLKL-----HPRLLTFASQLKGNFLHVKGKXTIVGSVIVG-----EALAAE 811
 LLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG EALAAE
 Sbjct: 744 LLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYGEALAAE 796

Query: 812 QTIKHVVACGLLENYLMEAEKVGFCQL---AKLREGISH-----GGMKHNTVVLIIQS 861
 QTIKH LMEAEKVGFCQL AKLREGISH GGMKHNTVV
 Sbjct: 797 QTIKH-----LMEAEKVGFCQLVVAAKLREGISHLIQSCGLGGMKHNTVV---- 842

Query: 862 MGWPNGWRQSERVTTDARAWKTFIGTVKNINIDL PFAAHLALLVA---SFFPSNVEQFSE 918
 MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSNVEQFSE
 Sbjct: 843 MGWPNGWRQSE----DARAWKTFIGTVR-VTT---AAHLALLVAKNISFFPSNVEQFSE 893

Query: 919 G---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK---ATFL 963
 G VWWIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK ATFL
 Sbjct: 894 GNIDVWWIVHDGGMLMLLPFLLLKQHKVWRKCSIRIFTVAQLEDNSI----QMKKDLATFL 949

Query: 964 YHLRIEAEVRIKDLLEVVRTLEMHSDISAYTYERHMRLSKMMEQRSQML-----TER 1016
 YHLRIEAEV EVV EMHSDISAYTYER + MMEQRSQML TER
 Sbjct: 950 YHLRIEAEV-----EVV---EMHSDISAYTYERTL----MMEQRSQMLRHMRLSKTER 996

Query: 1017 DRIAQLVKDRNSMLRLTSIGSDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM----- 1069
 DR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 997 DREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMTWTKDKY 1039

Query: 1070 --SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNMPGPPRN 1119
 SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRN
 Sbjct: 1040 MASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRN 1099

Query: 1120 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1155
 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS
 Sbjct: 1100 PEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1135

☐ >gi|41281645|ref|NP_598410.1| ☒ solute carrier family 12, member 6 [Mus musculus]
 gi|15042077|gb|AAK81895.1| ☒ K-C1 cotransporter 3a [Mus musculus]
 gi|27151686|sp|Q924N4|S126 MOUSE Solute carrier family 12 member 6 (Electroneutral
 cotransporter 3) (K-C1 cotransporter 3)
 Length = 1150

Score = 2466 bits (5808), Expect = 0.0

Identities = 907/1362 (66%), Positives = 923/1362 (67%), Gaps = 419/1362 (30%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPM 60
MHPPE TTKM+SVRFMVTPTKIDDIPGLSDTSPD SSRSSSRVRFSSRESVPETSRSEPM
Sbjct: 1 MHPPEATTKMSSVRFMVTPTKIDDIPGLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSONSGHKKAEDEYMDTRPGATTSLATVAL-----RTSHPQDVIED---- 111
SE+S GATTSLATVAL RTS+PQDV ED
Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTEDPSQN 95

Query: 112 -ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRM 155
ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNRM
Sbjct: 96 SITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRM 153

Query: 156 ANY----QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNI FGVTFMGVYI 202
ANY QGAKEHEEAENIT EGKKKPTK+PQMG LQNI FG V I
Sbjct: 154 ANYTNLTQGAKEHEEAENIT----EGKKKPTKSPQMGT FMGVYLPCLQNI FG V-----I 203

Query: 203 LFLRLLPCTWVVG TAGVLQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 262
LFLRL TWVVG TAG+LQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL
Sbjct: 204 LFLRL---TWVVG TAGILQAF AIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRAL 260

Query: 263 GPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDAL 310
GP EFGGAVGLCF AAAMYILGAI IVPRAAIF SDDAL
Sbjct: 261 GP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFRSDDAL 308

Query: 311 KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFASXFLACVIVSILAIYAGAIKSSFA 370
KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFAS FLACVIVSILAIYAGAIKSSFA
Sbjct: 309 KESAAMLNNMRVYGTAFLVLMVLVVF IGVRVYNKFASLFLACVIVSILAIYAGAIKSSFA 368

Query: 371 PPFFPVCMLGNRTLSS--IDVCSKTKEINNMT RHVPSK-----NATCDECNSS 416
PPFFPVCMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE
Sbjct: 369 PPFFPVCMLGNRTLSSRHL DICSKTKEVDNMT--VPSKLWGFFCNSSQFFNATCDE---- 422

Query: 417 YFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLV 472
YFVHNNV SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL
Sbjct: 423 YFVHNNV---ISIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGNLNHEYVLA 479

Query: 473 DPSAKITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS LWGFFV 532
D ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS FV
Sbjct: 480 D----ITTSFTLLVGIFFP SVTGIMAGSNRSGDLKDAQSIPIGTILAILTTS-----FV 530

Query: 533 YLSNVVLF GACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIVI 584
YLSNVVLF GACIEGVVLRDKFG DAVKGNLV PWVIVI
Sbjct: 531 YLSNVVLF GACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSPWVIVI 574

Query: 585 GS-----LQSLDNIITGAPFLRWALLRLLQAIK-----VFGH SKANGEPT-- 626
GS LQSL TGAP RLLQAIK VFGH SKANGEPT
Sbjct: 575 GSFFSTCGAGLQSL---TGAP-----RLLQAIKDNII PFLRVFGH SKANGEPTWA 622

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CA 664
GILIASLD LVAPI LSM CA
Sbjct: 623 LLLTAAIAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLACA 662

Query: 665 LQ-----RYYHWALSFMGMT PNWVNLRPRPRFSICLALMFI-----VAMV 705
LQ RYYHWALSFMGM SICLALMFI VAMV
Sbjct: 663 LQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISSWYYAIVAMV 708

Query: 706 IAGMIGAEEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP--- 759
 IAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP
 Sbjct: 709 IAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGP 752

Query: 760 KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKAGKGXTIVGSVIVG----- 805
 KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG
 Sbjct: 753 KNWRPQLLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENYG 805

Query: 806 EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHNT 855
 +ALAAEQTIKH LMEAEKVKGFCQL AKL+EGISH GGMKHNT
 Sbjct: 806 DALAAEQTIKH-----LMEAEKVKGFCQLVVAAKLKEGISHLIQSCGLGGMKHNT 855

Query: 856 VVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKKNINIDLPPFAAHLALLVA---SFFPSN 912
 VV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPSN
 Sbjct: 856 VV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNVSFFPSN 902

Query: 913 VEQFSEG---VWWIVHDGGMLMLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK- 959
 VEQFSEG V WIVHDGGMLMLL LKQHKVWRK TVAQLEDNSI QMK
 Sbjct: 903 VEQFSEGNIDVRWIVHDGGMLMLLPFLKQHKVWRKCSIRIFTVAQLEDNSI----QMKK 958

Query: 960 --ATFLYHLRIEAEVRIFKDLEVVRTLEMHDSDISAYTYERHMRLSKMMEQRSQML---- 1013
 ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQML
 Sbjct: 959 DLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL----MMEQRSQMLRHRM 1005

Query: 1014 ---TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTTWTKDKYMAQDLLHTAVYQEKVHM- 1069
 TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM
 Sbjct: 1006 LSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHMT 1048

Query: 1070 -----SRGQKAKSMEGF-----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLNM 1113
 SRGQK KSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLNM
 Sbjct: 1049 WTKDKYMASRGQKVKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNM 1108

Query: 1114 PGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1155
 PGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS
 Sbjct: 1109 PGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1150

☐ >gi|47124056|qb|AAH70107.1| **G** SLC12A6 protein [Homo sapiens]
 Length = 1156

Score = 2444 bits (5755), Expect = 0.0

Identities = 900/1336 (67%), Positives = 904/1336 (67%), Gaps = 419/1336 (31%)

Query: 27 GLSDTSPDXSSRSSSRVRFSSRESVPETSRSEPMSEMSDPPSDLSQNSGHKKAEGDEYMD 86
 GLSDTSPD SSRSSSRVRFSSRESVPETSRSEPMSEMS
 Sbjct: 33 GLSDTSPDLSSRSSSRVRFSSRESVPETSRSEPMSEMS----- 70

Query: 87 TRPGATTSLATVAL-----RTSHPQDVIED-----ITGEHSQLLDD----QRNAYLNNSN 132
 GATTSLATVAL RTSHPQDVIED ITGEHSQLLDD RNAYLNNSN
 Sbjct: 71 ---GATTSLATVALDPPSDRTSHPQDVIEDLSQNSITGEHSQLLDDGHKKARNAYLNNSN 127

Query: 133 YELFE-EESFDKNLA-----KVSSLLNRMANY---QGAKEHEEAENITNLTTTEG 177
 YE E +E FDKNLA KVSSLLNRMANY QGAKEHEEAENIT EG
 Sbjct: 128 YE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNLTQGAKEHEEAENIT----EG 181

Query: 178 KKKPTKTPQMG-----LQNI FGVT FMGVYILFLRLLPCTWVVG TAGVLQAF AIVLI 228
 KKKPTKTPQMG LQNI FGVT ILFLRL TWVVG TAGVLQAF AIVLI
 Sbjct: 182 KKKPTKTPQMGT FMGVYPPCLQNI FGVT ----ILFLRL---TWVVG TAGVLQAF AIVLI 232

Query: 229 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGTTFEIFLVYEFGGAVGLCF-- 286
 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP EFGGAVGLCF
 Sbjct: 233 CCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP-----EFGGAVGLCFYL 280

Query: 287 ----AAAMYILGAI-----IVPRAAIFHSDDALKESAAMLNNMRVYGTAFVLVLMVLVVF 336
 AAAMYILGAI IVPRAAIFHSDDALKESAAMLNNMRVYGTAFVLVLMVLVVF
 Sbjct: 281 GTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDALKESAAMLNNMRVYGTAFVLVLMVLVVF 340

Query: 337 IGVRYVNKFASXFLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSS--IDVCSKTK 394
 IGVRYVNKFAS FLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSS IDVCSKTK
 Sbjct: 341 IGVRYVNKFASLFLACVIVSILAIYAGAIKSSFAPPHPVCMLGNRTLSSRHIDVCSKTK 400

Query: 395 EINNMTTRHVPSK-----NATCDECNSSYFVHNNVQFFTSIQGIPGLASGIITE 442
 EINNMT VPSK NATCDE YFVHNNV TSIQGIPGLASGIITE
 Sbjct: 401 EINNMT--VPSKLWGFECNSSQFFNATCDE----YFVHNNV---TSIQGIPGLASGIITE 451

Query: 443 NLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKITTSFTLLVGIFFPSTVGIMA 498
 NLWSNYLPKGEIIEK SSDVLGSLNHEYVLVD ITTSFTLLVGIFFPSTVGIMA
 Sbjct: 452 NLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLVD---ITTSFTLLVGIFFPSTVGIMA 507

Query: 499 GSNRSGDLKDAQKSIPIGTILAILTTS LWGFFVYLSNVVLFGACIEGVVLRDKFGVGTL 558
 GSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVVLFGACIEGVVLRDKFG
 Sbjct: 508 GSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVVLFGACIEGVVLRDKFG---- 558

Query: 559 SWPSFFSTCGAGDAVKGNLV-----PWVIVIGS-----LQSLDNIITGAPPFLR 602
 DAVKGNLV PWVIVIGS LQSL TGAP
 Sbjct: 559 -----DAVKGNLVVGTLSWPSPWVIVIGSFFSTCGAGLQSL----TGAP---- 598

Query: 603 WALLRLLQAIK-----VFGHSKANGEPT-----GILIASLDFFLMCYLF 642
 RLLQAIK VFGHSKANGEPT GILIASLD
 Sbjct: 599 ----RLLQAIKDNIIIPFLRVFGHSKANGEPTWALLLTAAIAELGILIASLD----- 646

Query: 643 TLLRLTAALVAPIAELILSM-----CALQ-----RYYHWALSFMGM 678
 LVAPI LSM CALQ RYYHWALSFMGM
 Sbjct: 647 -----LVAPI----LSMFFLMCYLFVNLCALQTLLRTPNWRPRFRYYHWALSFMGM 694

Query: 679 TPNWVNLARPRPRFSICLALMFI-----VAMVIAGMIGA EKSSWYAIYKXIEYQSLS 731
 SICLALMFI VAMVIAGM IYK IEYQ
 Sbjct: 695 -----SICLALMFISSWYAIAMVIAGM-----IYKIEYQG-- 727

Query: 732 PHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQLLVLLKL-----HPRLLT 778
 E EWGDGIRGL AARFALLRLEEGP KNWRPQLLVLLKL HPRLLT
 Sbjct: 728 ---AEKEWGDGIRGLSLSAARFALLRLEEGPPHTKNWRPQLLVLLKLDEDLHVKHPRLLT 784

Query: 779 FASQLKGNFLHVKGAGXTIVG SVIVG-----EALAAEQTIKHVVACGLLENYLMEAE 831
 FASQLK AGKG TIVG SVIVG EALAAEQTIKH LMEAE
 Sbjct: 785 FASQLK-----AGKGLTIVG SVIVGNFLENYGEALAAEQTIKH-----LMEAE 827

Query: 832 KVKGFCQL---AKLREGISH-----GGMKHNTVVL IQSMGWPNQWRQSERVTTDARAW 881
 KVKGFCQL AKLREGISH GGMKHNTVV MGWPNGWRQSE DARAW
 Sbjct: 828 KVKGFCQLVVA AKLREGISHLIQSCGLGGMKHNTVV---MGWPNGWRQSE----DARAW 879

Query: 882 KTFIGTVKNINIDL PFAAHLALLVA---SFFPSNVEQFSEG---VWVIVHDGGM LMLL-- 933
 KTFIGTV+ + AAHLALLVA SFFPSNVEQFSEG VWVIVHDGGM LMLL
 Sbjct: 880 KTFIGTVR-VTT----AAHLALLVAKNISFFPSNVEQFSEGNIDVWVIVHDGGM LMLLPF 934

Query: 934 -LKQHKVWRK-----TVAQLEDNSISCSIQMK---ATFLYHLRIEAEVRIFKDLEVVRT 983
 LKQHKVWRK TVAQLEDNSI QMK ATFLYHLRIEAEV EVV
 Sbjct: 935 LLKQHKVWRKCSIRIFTVAQLEDNSI----QMKKDLATFLYHLRIEAEV-----EVV-- 982

Query: 984 LEMHSDISAYTYERHMLSKMMEQRSQML-----TERDRIAQLVKDRNSMLRLTSIG 1036
 EMHSDISAYTYER + MMEQRSQML TERDR AQLVKDRNSMLRLTSIG
 Sbjct: 983 -EMHSDISAYTYERTL----MMEQRSQMLRHMRLSKTERDREAQLVKDRNSMLRLTSIG 1037

Query: 1037 SDEDEETETTTWKDKYMAQDLLHTAVYQEKVHM-----SRGQKAKSMEGF----NM 1083
 SDEDEETET YQEKVHM SRGQKAKSMEGF NM
 Sbjct: 1038 SDEDEETET-----YQEKVHMTWTKDKYMASRGQKAKSMEGFQDLLNM 1080

Query: 1084 RPDQSNVRRM----KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGGLER 1139
 RPDQSNVRRM KLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGGLER
 Sbjct: 1081 RPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLNMPGPPRNPEGDENYMEFLEVLTGGLER 1140

Query: 1140 VLLVRGGGSEVITIYS 1155
 VLLVRGGGSEVITIYS
 Sbjct: 1141 VLLVRGGGSEVITIYS 1156

☐ >gi|33329256|gb|AAQ10028.1| ☒ K-C1 cotransporter KCC3a-S2 isoform [Homo sapiens]
☒ gi|33329254|gb|AAQ10027.1| ☒ K-C1 cotransporter KCC3a-S1 isoform [Homo sapiens]
 Length = 1091

Score = 2350 bits (5535), Expect = 0.0
 Identities = 868/1303 (66%), Positives = 872/1303 (66%), Gaps = 419/1303 (32%)

Query: 60 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL-----RTSHPQDVIED--- 111
 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVAL RTSHPQDVIED
 Sbjct: 1 MSEMSPDPSDLSONSGHKAEGDEYMDTRPGATTSLATVALDPPSDRTSHPQDVIEDLSQ 35

Query: 112 --ITGEHSQLLDD----QRNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNR 154
 ITGEHSQLLDD RNAYLNNSNYE E +E FDKNLA KVSSLLNR
 Sbjct: 36 NSITGEHSQLLDDGHKKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNR 93

Query: 155 MANY----QGAKEHEEAENITNLTTGKPKTKTPQMG-----LQNIFGVTFMGVY 201
 MANY QGAKEHEEAENIT EGKPKTKTPQMG LQNIFGV
 Sbjct: 94 MANYTNLTQGAKEHEEAENIT----EGKPKTKTPQMGTFMGVYLPCLQNIFGV----- 143

Query: 202 ILFLRLLPCTWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 261
 ILFLRL TWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA
 Sbjct: 144 ILFLRL---TWVVGTAFLVLAFAIVLICCCCTMLTAISMSAIATNGVVPAGGSYFMISRA 200

Query: 262 LGPYLGTTFEIFLVYEFGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDA 309
 LGP EFGGAVGLCF AAAMYILGAI IVPRAAIFHSDDA
 Sbjct: 201 LGP-----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFHSDDA 248

Query: 310 LKESAAMLNNMRVYGTAFVLVLMVLVVFIVGVYVNFASXFLACVIVSILAIYAGAIKSSF 369
 LKESAAMLNNMRVYGTAFVLVLMVLVVFIVGVYVNFAS FLACVIVSILAIYAGAIKSSF
 Sbjct: 249 LKESAAMLNNMRVYGTAFVLVLMVLVVFIVGVYVNFASLFLACVIVSILAIYAGAIKSSF 308

Query: 370 APPHFPVCMLGNRTLSS--IDVCSKTKEINNMTTRHVPSK-----NATCDECNS 415
 APPHFPVCMLGNRTLSS IDVCSKTKEINNMT VPSK NATCDE
 Sbjct: 309 APPHFPVCMLGNRTLSSRHIDVCSKTKEINNMT--VPSKLWGFFCNSSQFFNATCDE--- 363

Query: 416 SYFVHNNVQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVL 471
 YFVHNNV TSIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLGSLNHEYVL
 Sbjct: 364 -YFVHNNV---TSIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVL 419

Query: 472 VDPSAKITTSFTLLVGIFFPSTGIMAGSNRSGDLKDAQKSIPIGTILAILTTSLWGFFF 531
 VD ITTSFTLLVGIFFPSTGIMAGSNRSGDLKDAQKSIPIGTILAILTT F

Sbjct: 420 VD----ITTSFTLLVGIFFPSVTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----F 470

Query: 532 VYLSNVVLFGACIEGVVLRDKFGVGTLSWPSFFSTCGAGDAVKGNLV-----PWVIV 583
VYLSNVVLFGACIEGVVLRDKFG DAVKGNLV PWVIV

Sbjct: 471 VYLSNVVLFGACIEGVVLRDKFG-----DAVKGNLVVGTLSWPSFWVIV 514

Query: 584 IGS-----LQSLDNIITGAPPFLRWALLRLLQAIK-----VFGHSKANGEPT- 626
IGS LQSL TGAP RLLQAIK VFGHSKANGEPT

Sbjct: 515 IGSFFSTCGAGLQSL----TGAP-----RLLQAIKDNIIIPFLRVFGHSKANGEPTW 562

Query: 627 -----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----C 663
GILIASLD LVAPI LSM C

Sbjct: 563 ALLLTAAIAELGILIASLD-----LVAPI----LSMFFLMCYLFVNLC 602

Query: 664 ALQ-----RYYHWALSFMGMTPNWVNLRPRRFSICLALMFI-----VAM 704
ALQ RYYHWALSFMGM SICLALMFI VAM

Sbjct: 603 ALQTLRLTPNWRPRFRYYHWALSFMGM-----SICLALMFISWYYAIVAM 648

Query: 705 VIAGMIGAEEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP-- 759
VIAGM IYK IEYQ E EWGDGIRGL AARFALLRLEEGP

Sbjct: 649 VIAGM-----IYKIEYQG-----AEKEWGDGIRGLSLSAARFALLRLEEGPPH 692

Query: 760 -KNWRPQLLVLLKL-----HPRLLTFASQLKGNFLHVKGXGTIVGSVIVG----- 805
KNWRPQLLVLLKL HPRLLTFASQLK AGKG TIVGSVIVG

Sbjct: 693 TKNWRPQLLVLLKLDEDLHVKHPRLLTFASQLK-----AGKGLTIVGSVIVGNFLENY 745

Query: 806 -EALAAEQTIKHVVACGLLENYLMEAEKVKGFCQL---AKLREGISH-----GGMKHN 854
EALAAEQTIKH LMEAEKVKGFCQL AKLREGISH GGMKHN

Sbjct: 746 GEALAAEQTIKH-----LMEAEKVKGFCQLVVAAKLREGISHLIQSCGLGGMKHN 795

Query: 855 TVVLIQSMGWPNGWRQSERVTTDARAWKTFIGTVKNINIDLPPAAHLALLVA---SFFPS 911
TVV MGWPNGWRQSE DARAWKTFIGTV+ + AAHLALLVA SFFPS

Sbjct: 796 TVV----MGWPNGWRQSE----DARAWKTFIGTVR-VTT----AAHLALLVAKNISFFPS 842

Query: 912 NVEQFSEG---VWWIVHDGGMMLLL---LKQHKVWRK-----TVAQLEDNSISCSIQMK 959
NVEQFSEG VWWIVHDGGMMLLL LKQHKVWRK TVAQLEDNSI QMK

Sbjct: 843 NVEQFSEGNIDVWWIVHDGGMMLLLPFLKQHKVWRKCSIRIFTVAQLEDNSI----QMK 898

Query: 960 ---ATFLYHLRIEAEVRIFKOLEVVRTLEMHDSDISAYTYERHMRSLKMMEQRSQML--- 1013
ATFLYHLRIEAEV EVV EMHDSDISAYTYER + MMEQRSQML

Sbjct: 899 KDLATFLYHLRIEAEV-----EVV---EMHDSDISAYTYERTL----MMEQRSQMLRHM 945

Query: 1014 ----TERDRIAQLVKDRNSMLRLTSIGSDEDEETETTWTCKDYMAQDLLHTAVYQEKVHM 1069
TERDR AQLVKDRNSMLRLTSIGSDEDEETET YQEKVHM

Sbjct: 946 RLSKTERDREAQLVKDRNSMLRLTSIGSDEDEETET-----YQEKVHM 988

Query: 1070 -----SRGQKAKSMEGF----NMRPDQSNVRRM----KLNEVIVNKSHEAKLVLLN 1112
SRGQKAKSMEGF NMRPDQSNVRRM KLNEVIVNKSHEAKLVLLN

Sbjct: 989 TWTCKDYMASRGQKAKSMEGFQDLLNMRPDQSNVRRMHTAVKLNEVIVNKSHEAKLVLLN 1048

Query: 1113 MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1155
MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS

Sbjct: 1049 MPGPPRNPEGDENYMEFLEVLTEGLERVLLVRGGGSEVITIYS 1091

☐ >gi|38565928|qb|AAH62099.1| Unknown (protein for MGC:69652) [Mus musculus]
Length = 1106

Score = 2345 bits (5523), Expect = 0.0

Identities = 868/1326 (65%), Positives = 884/1326 (66%), Gaps = 422/1326 (31%)

Query: 1 MHPPETTTKMASVRFMVTPTKIDDIPGLSDTSPDXSSRSSRVRFSSRESVPETSRSEPM 60
 MHPPE TTKM+SVRFMVTPTKIDDIPGLSDTSPD SSRSSRVRFSSRESVPETSRSEPM
 Sbjct: 1 MHPPEATTKMSSVRFMVTPTKIDDIPGLSDTSPDLSSRSSRVRFSSRESVPETSRSEPM 60

Query: 61 SEMSDPPSDLSQNSGHKKAEGDEYMDTRPGATTSLATVAL-----RTSHPDQDVIEDITGE 115
 SE+S GATTSLATVAL RTS+PDV ED
 Sbjct: 61 SELS-----GATTSLATVALDPSSDRTSNPQDVTED---- 91

Query: 116 HSQLLDDQ---RNAYLNNSNYELFE-EESFDKNLA-----KVSSLLNRMANY--- 158
 D RNAYLNNSNYE E +E FDKNLA KVSSLLNRMANY
 Sbjct: 92 -----DGHKARNAYLNNSNYE--EGDEYFDKNLALFEEEMDTRPKVSSLLNRMANYTNL 144

Query: 159 -QGAKEHEEAENITNLTTEGKKKPTKTPQMG-----LQNIFGVTFMGVYILFLRL 208
 QGAKEHEEAENIT EGKKKPTK+PQMG LQNIFGV ILFLRL
 Sbjct: 145 TQGAKEHEEAENIT----EGKKKPTKSPQMGTFMGVYLPCLQNIFGV-----ILFLRL- 193

Query: 209 PCTWVVGTTAGVLQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGPYLGT 268
 TWVVGTTAG+LQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP
 Sbjct: 194 --TWVVGTTAGILQAFVILICCCCTMLTAISMSAIATNGVVPAGGSYFMISRALGP---- 247

Query: 269 TFEIFLVYFEGGAVGLCF-----AAAMYILGAI-----IVPRAAIFHSDDALKESAAM 316
 EFGGAVGLCF AAAMYILGAI IVPRAAIF SDDALKESAAM
 Sbjct: 248 -----EFGGAVGLCFYLGTTFAAAMYILGAIEIFLVYIVPRAAIFRSDDALKESAAM 299

Query: 317 LNNMRVYGTAFVLMVLVVFVIGVRYVNFASFACVIVSILAIYAGAIKSSFPAPHPFV 376
 LNNMRVYGTAFVLMVLVVFVIGVRYVNFASFACVIVSILAIYAGAIKSSFPAPHPFV
 Sbjct: 300 LNNMRVYGTAFVLMVLVVFVIGVRYVNFASFACVIVSILAIYAGAIKSSFPAPHPFV 359

Query: 377 CMLGNRTLSS--IDVCSKTKEINNMTRHVPSK-----NATCDECNSSYFVHNN 422
 CMLGNRTLSS +D+CSKTKE++NMT VPSK NATCDE YFVHNN
 Sbjct: 360 CMLGNRTLSSRHLDCSKTKEVDNMT--VPSKLWGFFCNSSQFFNATCDE----YFVHNN 413

Query: 423 VQFFTSIQGIPGLASGIITENLWSNYLPKGEIIEK----SSDVLGSLNHEYVLVDPSAKI 478
 V SIQGIPGLASGIITENLWSNYLPKGEIIEK SSDVLG+LNHEYVL D I
 Sbjct: 414 V---ISIQGIPGLASGIITENLWSNYLPKGEIIEKPSAKSSDVLGSLNHEYVLAD----I 466

Query: 479 TTSTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTSWLGFFVYLSNVV 538
 TTSTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS FVYLSNVV
 Sbjct: 467 TTSTLLVGIFFPSTGTGIMAGSNRSGDLKDAQKSIPIGTILAILTTS-----FVYLSNVV 521

Query: 539 LFGACIEGVVLRDKFVGTLSPWPSFFSTCGAGDAVKGNLV-----PWVIVIGS---- 586
 LFGACIEGVVLRDKF DAVKGNLV PWVIVIGS
 Sbjct: 522 LFGACIEGVVLRDKF-----DAVKGNLVVGTLSWPSPWVIVIGSFFST 565

Query: 587 ----LQSLDNIITGAPPFLRWALLRLQAIK-----VFGHSKANGEPT----- 626
 LQSL TGAP RLLQAIK VFGHSKANGEPT
 Sbjct: 566 CGAGLQSL----TGAP-----RLLQAIKDNIIPFLRVFGHSKANGEPTWALLLTAA 613

Query: 627 ----GILIASLDFFLMCYLFTLLRLTAALVAPIAELILSM-----CALQ---- 666
 GILIASLD LVAPI LSM CALQ
 Sbjct: 614 IAEKGILIASLD-----LVAPI---LSMFFLMCYLFVNLCALQTLLR 653

Query: 667 -----RYYHWALSFMGMTPNWVNLRPRPRFSICLALMFI-----VAMVIAGMIG 711
 RYYHWALSFMGMT SICLALMFI VAMVIAGM
 Sbjct: 654 TPNWRPRFRYYHWALSFMGMT-----SICLALMFISSWYYAIVAMVIAGM-- 697

Query: 712 AEKSSWYYAIYKXIEYQSLSPHTDEDEWGDGIRGL---AARFALLRLEEGP---KNWRPQ 765
 IYK IEYQ E EWGDGIRGL AARFALLRLEEGP KNWRPQ